Pending Claims:

Claims 1-9. (Canceled)

Claim 10. (Previously Presented):   A method for identifying a polypeptide that binds to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a)   providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b)   contacting the support to which the overlapping peptides are covalently attached with a mixture of polypeptides under conditions enabling binding between the peptides on the support and a polypeptide of the mixture;

(c)   washing the support to remove unbound polypeptides of the mixture; and

(d)   identifying a polypeptide that is retained on the support,

wherein the polypeptide that is retained on the support is the polypeptide that binds to the peptide in the chosen protein.

Claim 11. (Previously Presented):   The method of claim 10, wherein the polypeptide that binds to the peptide in the chosen protein binds to a high affinity domain of the chosen protein.

Claim 12. (Previously Presented):   The method of claim 10, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 13. (Previously Presented):   The method of claim 10, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 14. (Previously Presented):   The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 15. (Previously Presented):   The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 16. (Previously Presented):   The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 17. (Previously Presented):   The method of claim 10, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 18. (Canceled)

Claim 19. (Previously Presented):   The method of claim 10, wherein the mixture of polypeptides comprises a cell lysate.

Claim 20. (Previously Presented):   The method of claim 10, wherein the chosen protein is human P-glycoprotein 1.

Claims 21-22. (Canceled)

Claim 23. (Previously Presented):   The method of claim 20, wherein the polypeptide is tubulin.

Claim 24. (Previously Presented):   The method of claim 10, wherein the chosen protein is human P-glycoprotein 3.

Claim 25. (Canceled)

Claim 26. (Previously Presented):   A method for identifying a peptide in a chosen protein that binds to a polypeptide, wherein said polypeptide is not an antibody, the method comprising:

(a)   providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b)   contacting the support to which the overlapping peptides are attached with the polypeptide under conditions enabling binding between the peptide attached to the support and the polypeptide;

(c)   washing the support to remove unbound polypeptide; and

(d)   identifying the peptide attached to the support that binds to the polypeptide.

Claim 27. (Previously Presented):   The method of claim 26, wherein the peptide attached to the support that binds to the polypeptide is comprised within a high affinity domain of the chosen protein.

Claim 28. (Canceled)

Claim 29. (Previously Presented):   The method of claim 26, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 30. (Previously Presented):   The method of claim 26, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 31. (Previously Presented):   The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 32. (Previously Presented):   The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 33. (Previously Presented):   The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 34. (Previously Presented):   The method of claim 26, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 35. (Canceled)

Claim 36. (Previously Presented):   The method of claim 26, wherein the chosen protein is human P-glycoprotein 1.

Claims 37-38. (Canceled)

Claim 39. (Previously Presented):   The method of claim 36, wherein the polypeptide is tubulin.

Claim 40. (Previously Presented):   The method of claim 26, wherein the chosen protein is human P-glycoprotein 3.

Claim 41. (Canceled)

Claim 42. (Withdrawn):   A method of identifying a compound that modulates the binding of a polypeptide to a peptide in a chosen protein, wherein said polypeptide is not an antibody, comprising:

(a)   providing a set of overlapping peptides spanning a complete sequence of at least a domain of the chosen protein, the set of overlapping peptides being covalently attached to a support;

(b)   contacting the support to which the overlapping peptides are attached with a candidate compound and the polypeptide under conditions enabling binding between the peptide attached to the support and the polypeptide;

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(c)   washing the support to remove unbound polypeptides of the mixture; and

(d)   detecting binding of the polypeptide to the peptide attached to the support,

wherein a change in the binding of the polypeptide to the peptide attached to the support in the presence of the candidate compound compared to the binding of the polypeptide to the peptide attached to the support in the absence of the candidate compound identifies the candidate compound as a compound that modulates binding of the polypeptide to the peptide in the chosen protein.

Claim 43. (Withdrawn):   The method of claim 42, wherein the domain of the chosen protein is a high affinity domain of the chosen protein.

Claim 44. (Withdrawn):   The method of claim 42, wherein the polypeptide is known to bind to the chosen protein.

Claim 45. (Withdrawn):   The method of claim 42, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 46. (Withdrawn):   The method of claim 42, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 47. (Withdrawn):   The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 48. (Withdrawn):   The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 49. (Withdrawn):   The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 50. (Withdrawn):   The method of claim 42, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 51. (Canceled)

Claim 52. (Withdrawn):   The method of claim 42, wherein the chosen protein is human P-glycoprotein 1.

Claims 53-54. (Canceled)

Claim 55. (Withdrawn):   The method of claim 52, wherein the polypeptide is tubulin.

Claim 56. (Withdrawn):   The method of claim 42, wherein the chosen protein is human P-glycoprotein 3.

Claim 57. (Canceled)

Claim 58. (Withdrawn):   A support to which are attached overlapping peptides spanning a complete sequence of at least a domain of a protein.

Claim 59. (Withdrawn):   The support of claim 58, wherein the domain of the protein is a high affinity domain of the protein.

Claim 60. (Withdrawn):   The support of claim 58, wherein the overlapping peptides span the complete sequence of the entire protein.

Claim 61. (Withdrawn):   The support of claim 58, wherein the support is selected from the group consisting of a chip, a bead, and a plate.

Claim 62. (Withdrawn):   The support of claim 58, wherein the overlapping peptides attached to the support are synthesized synthetically using the amino acid sequence of the chosen protein.

Claim 63. (Withdrawn):   The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 15 amino acids in length.

Claim 64. (Withdrawn):   The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 12 amino acids in length.

Claim 65. (Withdrawn):   The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 10 amino acids in length.

Claim 66. (Withdrawn):   The support of claim 58, wherein each of the overlapping peptides attached to the support is from about 5 amino acids to about 7 amino acids in length.

Claim 67. (Withdrawn):   The support of claim 58, wherein the overlapping peptides is covalently attached to the support.

Claim 68. (Withdrawn):   The support of claim 58, wherein a polypeptide that binds to a peptide attached to the support is identified as a polypeptide that binds to the protein.

Claim 69. (Withdrawn):   The support of claim 58, wherein the chosen protein is human P-glycoprotein 1.

Claims 70-71. (Canceled)

Claim 72. (Withdrawn):   The support of claim 58, wherein the chosen protein is human P-glycoprotein 3.

Claims 73-74. (Canceled)

Claim 75. (Previously Presented):   The method of claim 26, further comprising identifying the peptide in the chosen protein to which the polypeptide binds the chosen protein.

Claim 76. (Previously Presented):   The method of claim 75, wherein the peptide in the chosen protein to which the polypeptide binds is identified by its position on the support.

Claim 77. (Previously Presented): The method of claim 10, wherein identifying a polypeptide that is retained on the support is accomplished by a method selected from the group consisting of labeling the polypeptide and identifying the labeled polypeptide, mass spectrometry, 2-D gel electrophoresis, and combinations thereof.

Claim 78. (Previously Presented): The method of claim 26, wherein identifying the peptide attached to the support that binds to the polypeptide is accomplished by a method selected from the group consisting of labeling the polypeptide and identifying the labeled polypeptide, mass spectrometry, 2-D gel electrophoresis, and combinations thereof.